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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/029,115	10/19/2001	Ying Luo	A-70229/RMS/DHR	2856

20350 7590 09/02/2004

TOWNSEND AND TOWNSEND AND CREW, LLP  
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SAN FRANCISCO, CA 94111-3834

EXAMINER

GIBBS, TERRA C

ART UNIT	PAPER NUMBER
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1635

DATE MAILED: 09/02/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

## Office Action Summary

### Application No.

10/029,115

### Applicant(s)

LUO ET AL.

### Examiner

Terra C. Gibbs

### Art Unit

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 14 June 2004.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 2,3 and 16-26 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 2,3 and 16-26 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

### Attachment(s)

- ☐ Notice of References Cited (PTO-892)
- ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)  
Paper No(s)/Mail Date \_\_\_\_\_
- ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_\_
- ☐ Notice of Informal Patent Application (PTO-152)
- ☒ Other: Sequence search alignments.

### **DETAILED ACTION**

This Office Action is a response to Applicants Amendment and Remarks filed June 14, 2004.

Claims 1 and 4-15 have been canceled. Claims 2, 3, 16, and 17 have been amended. New claims 21-26 are acknowledged.

Claims 2, 3, and 16-26 have been examined on the merits.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

### ***Claim Rejections - 35 USC § 112***

In the previous Office Action mailed March 9, 2004, claims 2 and 3 were rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. **This rejection is maintained** for the reasons of record set forth in the previous Office Action mailed March 9, 2004.

### ***Response to Arguments***

In response to this rejection, Applicants argue that claim 2 is now amended to recite a nucleic acid sequence having at least about 95% identity to SEQ ID NO:1, 3, or 5. Applicants argue that claim 2 has also been amended to recite that the nucleic acid, *and not its complement*, encodes a MINK3 protein.

This argument has been fully considered, but is not found persuasive because claims 2 and 3 still read on the *complement* of SEQ ID NO:1, 3, or 5 encoding a MINK3 protein. For

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example, claims 2 and 3 are drawn to a recombinant nucleic acid, comprising a nucleic acid sequence having at least 95% identity to a nucleic acid sequences of SEQ ID NO:1, 3, and 5, **or complements thereof**, wherein said recombinant nucleic acid encodes a MINK3 protein. Therefore, the issue is would the *complement* of a recombinant nucleic acid comprising SEQ ID NOs:1, 3, and 5, encode a MINK3 protein as claimed? The Specification discloses SEQ ID NOs:1, 3, and 5 encode a MINK3 protein, but has not described a recombinant nucleic acid comprising SEQ ID NOs:1, 3, and 5, **or complements thereof**, which encode a MINK3 protein.

Applicant's amendment necessitated the new ground(s) of rejection presented below:

***Claim Rejections - 35 USC § 112***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

New claim 21 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. **This is a new written description rejection.**

Claim 21 is drawn to a recombinant nucleic acid, comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of

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SEQ ID NOs: 1, 3, and 5, **or complements thereof**, wherein said recombinant nucleic acid encodes a MINK3 protein.

The issue is would the *complement* of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, encode a MINK3 protein as claimed? The instant Specification teaches SEQ ID NOs:1, 3, and 5 encode a MINK3 protein. Applicants have not described a complement of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein.

Applicant is referred to the Guidelines on Written Description, published at FR 66(4) 1099-1111 (January 5, 2001) (also available at [www.uspto.gov](http://www.uspto.gov)). The following passage is particularly relevant:

The written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species, by actual reduction to practice, reduction to drawings, or by disclosure of relevant identifying characteristics, i.e. structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between structure and function structure, or by a combination of such identifying characteristics, sufficient to show the Applicant was in possession of the claimed genus.

A "representative number of species" means that the species which are adequately described are representative of the entire genus. Thus, when there is substantial variation within a genus, one must describe a sufficient number of species to reflect the variation within the genus. What constitutes a "representative number" is an inverse function of the skill and knowledge in the art. Satisfactory disclosure of a "representative number" depends on whether one of skill in the art would recognize that Applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed. In an unpredictable art, adequate written description of a genus which embraces widely variant species cannot be achieved by disclosing only one species within the genus.

The central issue of this rejection is whether Applicant has described a sufficient number of species to adequately represent the genus of complement recombinant nucleic acids comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence

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selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein. It is unclear how the *complement* of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, will encode a MINK3 protein as claimed. It is recognized in the prior art that the function of a protein depends on the sequence of its amino acids in a certain pattern, conformation of the protein due to the amino acid sequence, and the functional properties of the different parts of the protein (see second paragraph in Rudinger J in Peptide Hormones. Editor Parsons JA. Pages 1-7, 1976, University Park Press, Baltimore). Rudinger further add, "The significance of particular amino acids and sequences for different aspects of biological activity can not be predicted *a priori* but must be determined from case to case by painstaking experimental study" (see conclusion on page 6).

In summary, the Specification teaches SEQ ID NOs:1, 3, and 5 encode a MINK3 protein, but has not described the complement of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein. In view of the number of disclosed species, and the failure to provide the structure and physical properties of the complement of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein, which would allow one to accurately predict the recombinant nucleic acids which possess such activity, one of skill in the art would conclude that Applicant was not in possession of the claimed invention at the time of filing.

***Claim Rejections - 35 USC § 102***

In the previous Office Action mailed March 9, 2004, claims 2, 3, and 16-18 were rejected under 35 U.S.C. 102(b) as being anticipated by Ippeita et al. (FEBS Letters, 2000 Vol. 469:19-23). **This rejection is maintained** for the reasons of record set forth in the previous Office Action.

***Response to Arguments***

In response to this rejection, Applicants argument is three-fold. First, Applicants argue that to anticipate a claim, the reference must teach every element of the claims. Second, Applicants argue that claim 2 has been amended to recite a nucleic acid having greater than about 95% identity to SEQ ID NO:1, 3, or 5, and this amendment obviates the instant rejection. Third, Applicants argue that claim 16 is directed to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. Applicants argue that the Office Action appears to incorrectly assert that the MINK3 polypeptide of SEQ ID NO:2 of the instant invention contains the full amino acid sequence of the MINK1 protein of Ippeita et al. in combination with additional amino sequences. Applicants contend that nucleobases 1738-1798 of MINK1 are not present in SEQ ID NO:1, and because SEQ ID NO:2 does not include all the sequences of the cited MINK1, claim 16 and dependent claims 17-20 are not anticipated by Ippeita et al.

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This argument has been fully considered, but is not found persuasive. First regarding Applicants first argument, the cited art teaches every element of the instant claims. For example, [and in response to Applicants second argument] claim 2 has been amended to recite a recombinant nucleic acid, comprising a nucleic acid sequence having at least 95% identity to a nucleic acid sequences of SEQ ID NO:1, 3, and 5, or complements thereof, wherein said recombinant nucleic acid encodes a MINK3 protein. Ippeita et al. disclose the molecular cloning of MINK1 (see Figure 2). The nucleotide sequence of MINK1 is over 96% identical to SEQ ID NO:1 of the instant invention (see attached sequence alignment), and thus meets the limitations of claim 2 and dependent claim 3. Regarding Applicants third argument, claim 16 is drawn to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. The MINK1 disclosure of Ippeita et al. further meets the limitations of claim 16 because the amino acid sequence of MINK1 is almost 99% identical to SEQ ID NO:2 of the instant invention (see attached sequence alignment), and thus meets the limitations of claim 16 and dependent claims 17 and 18.

Therefore, Ippeita et al. anticipate claims 2, 3, and 16-18.

In the previous Office Action mailed March 9, 2004, claims 2, 3, and 16-18 were rejected under 35 U.S.C. 102(b) as being anticipated by Plowman et al. [U.S. Patent No. 6,656,716] ('716 Patent). **This rejection is maintained** for the reasons of record set forth in the previous Office Action.



*Response to Arguments*

In response to this rejection, Applicants argument is three-fold. First, Applicants argue that to anticipate a claim, the reference must teach every element of the claims. Second, Applicants argue that claim 2 has been amended to recite a nucleic acid having greater than about 95% identity to SEQ ID NO:1, 3, or 5, and this amendment obviates the instant rejection. Third, Applicants argue that claim 16 is directed to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. Applicants argue that the Office Action appears to incorrectly assert that the MINK3 polypeptide of SEQ ID NO:2 of the instant invention contains the full amino acid sequence of the ZC3 protein of Plowman et al. in combination with additional amino sequences. Applicants contend that residues 582-602 are not present in SEQ ID NO:2 and because SEQ ID NO:2 does not include all the sequences of the cited ZC3, claim 16 and dependent claims 17-20 are not anticipated by Plowman et al.

This argument has been fully considered, but is not found persuasive. First regarding Applicants first argument, the cited art teaches every element of the instant claims. For example, [and in response to Applicants second argument] claim 2 has been amended to recite a recombinant nucleic acid, comprising a nucleic acid sequence having at least 95% identity to a nucleic acid sequences of SEQ ID NO:1, 3, and 5, or complements thereof, wherein said recombinant nucleic acid encodes a MINK3 protein. The '716 Patent discloses the nucleotide sequence of human ZC3 (see SEQ ID NO:11 and Figure 9J), which is over 95% identical to SEQ ID NO:1 of the instant invention (see attached sequence alignment), and thus meets the

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limitations of claim 2 and dependent claim 3. Regarding Applicants third argument, claim 16 is drawn to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. The ZC3 disclosure of Plowman et al. further meets the limitations of claim 16 because the amino acid sequence of ZC3 is almost 96% identical to SEQ ID NO:2 of the instant invention (see attached sequence alignment), and thus meets the limitations of claim 16 and dependent claims 17 and 18.

Therefore, Plowman et al. anticipate claims 2, 3, and 16-18.

Applicant's amendment necessitated the new ground(s) of rejection presented below:

***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claim 19, 20, and new claims 22-26 are rejected under 35 U.S.C. 102(b) as being anticipated by Ippeita et al. (FEBS Letters, 2000 Vol. 469:19-23). **This is a new rejection.**

Claim 19 is drawn to a method of making a MINK3 protein comprising culturing a host cell comprising a recombinant nucleic acid, comprising a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of SEQ ID NOs: 2, 4, and 6, under conditions suitable for

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the expression of MINK3. Claim 20 is dependent on claim 19 and includes all the limitations of claim 19, with the further step of isolating the MINK3 protein. Claim 22 is drawn to a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence having at least 98% identity to an amino acid selected from the group consisting of SEQ ID NOs: 2, 4, and 6. Claim 23 is drawn to a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, and 6. Claims 24-26 are drawn to a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of SEQ ID NOs: 2, 4, and 6, wherein the MINK3 protein activates a(n) JNK and ERK, and binds to a Nck protein.

Ippeita et al. disclose the molecular cloning of MINK1 (see Figure 2). The nucleotide sequence of MINK1 is over 96% identical to SEQ ID NO:1 of the instant invention (see attached sequence alignment), while the amino acid sequence of MINK1 is over 99% identical to SEQ ID NO:2 of the instant invention (see attached sequence alignment), and thus meets the limitations of claims 22 and 23. Ippeita et al. disclose full length MINK1 was cloned into a pCMV expression vector and transiently expressed in HEK 293 cells (see Figure 5A) and thus meets the limitations of claims 19 and 20. Ippeita et al. further disclose the kinase activity of MINK1, and show that MINK1 activates JNK and ERK proteins (see Figures 5B and 5D, respectively). It is noted that Ippeita et al. do not disclose that MINK1 binds to a Nck protein. However, at page 20, second column, Ippeita et al. disclose that it is likely that MINK1 interacts with Nck because the two share conserved binding regions. Therefore, absent evidence to the contrary, MINK1 binds to a Nck protein.

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Therefore, claims 19, 20, and 22-26 are anticipated by Ippeita et al.

### ***Conclusion***

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire **THREE MONTHS** from the mailing date of this action. In the event a first reply is filed within **TWO MONTHS** of the mailing date of this final action and the advisory action is not mailed until after the end of the **THREE-MONTH** shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than **SIX MONTHS** from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Terra C. Gibbs whose telephone number is (571) 272-0758. The examiner can normally be reached on M-F 9:00-5:00.

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If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John L. LeGuyader can be reached on (571) 272-0760. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

tcg

September 1, 2004



JOHN L. LeGUYADER  
SUPERVISORY PATENT EXAMINER  
TECHNOLOGY CENTER 1600

# Sequence search alignment. ..

## Applicants Copy

### ALIGNMENTS

#### RESULT 1

#### M4K6\_HUMAN

ID M4K6\_HUMAN STANDARD; PRT; 1332 AA.  
AC Q8N4C8; Q9P1X1; Q9P2R8;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Mitogen-activated protein kinase kinase kinase 6 (EC 2.7.1.37)  
DE (MAPK/ERK kinase kinase 6) (MEK kinase kinase 6) (MEKKK 6)  
DE (Misshapen/NIK-related kinase) (GCK family kinase MINK).  
GN MAP4K6 OR MINK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Brain;  
RX MEDLINE=20175403; PubMed=10708748;  
RA Dan I., Watanabe N.M., Kobayashi T., Yamashita-Suzuki K., Fukagaya Y.,  
RA Kajikawa E., Kimura W.K., Nakashima T.M., Matsumoto K.,  
RA Ninomiya-Tsuji J., Kusumi A.;  
RT "Molecular cloning of MINK, a novel member of mammalian GCK family  
RT kinases, which is up-regulated during postnatal mouse cerebral  
RT development.";  
RL FEBS Lett. 469:19-23(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Serine/threonine kinase that may play a role in the  
CC response to environmental stress. Appears to act upstream of the  
CC c-jun N-terminal pathway (By similarity).  
CC -!- FUNCTION: May play a role in the development of the brain (By  
CC similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + a prptein = ADP + a

Applicants Copy

## RESULT 1

Query Match 96.1%; Score 6659; DB 4; Length 1326;  
Best Local Similarity 95.8%; Pred. No. 0;  
Matches 1270; Conservative 3; Mismatches 3; Indels 50; Gaps 3;

Qy	36	YGQVYGRHVKTKQLAAIKVMDVTEDEEEI KQEI NMLKKYSHHRNIATYYGAFIKKSPP	95
Db	2	FGEVYGRHVKTKQLAAIKVMDVTEDEEEI KQEI NMLKKYSHHRNIATYYGAFIKKSPP	61
Qy	96	GNDQDLWLVMEFCGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHLHAHKVHIRDIK	155
Db	62	GNDQDLWLVMEFCGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHLHAHKVHIRDIK	121
Qy	156	GQNVLLTENA EVKLVD FGVSAQLDRTVGRNRTFIGTPYWMAPEVIACDENPDATYDYRS	215
Db	122	GQNVLLTENA EVKLVD FGVSAQLDRTVGRNRTFIGTPYWMAPEVIACDENPDATYDYRS	181
Qy	216	IWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNP PRLKSKKWSKKFIDFIDTCLIKTYL	275
Db	182	IWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNP PRLKSKKWSKKFIDFIDTCLIKTYL	241
Qy	276	SRPPTQLLKFPFIRDPQTERQVRIQLKDHIDRSRKKRGEKEETEY EYSGSEEDDSHGE	335
Db	242	SRPPTQLLKFPFIRDPQTERQVRIQLKDHIDRSRKKRGEKEETEY EYSGSEEDDSHGE	301
Qy	336	EGEPSSIMNVPGESTLRREFLR LQENKNSNSEAL KQQQQQLQQQQORDPEAHIKHLHQRQ	395

u.s-10-029-1.

Db	302	EGEPSSIMVPGESTLRREFLRLQENKSNSEALKQOQQQLQQQQQORDPEAHIKHLLHQRO	361
Qy	396	RRIEEQKEERRRVVEEQRREREQRKLQKEQEQRRLLEDQMALRREEERRQAEREQ	449
Db	362	RRIEEQKEERRRVVEEQRREREQRKLQKEQEQRRLLEDQMALRREEERRQAEREQEYIRHR	421
Qy	450	-----EYKRKQLEEQRQSERLQRLQOEHAYLKSLQQQQQQQ	486
Db	422	LEEEQRQLEILQQOQLQEALLEYKRKQLEEQRQSERLQRLQOEHAYLKSLQQQQQQQ	481
Qy	487	QLQKQQQQQLLPGRDKPLYHYGRGMNPADKPAWAREVEERTRMNKQONSPLAKSKPGSTG	546
Db	482	QLQKQQQQQLLPGRDKPLYHYGRGMNPADKPAWAREVEERTRMNKQONSPLAKSKPGSTG	541
Qy	547	PEPPIQASPGPPGPLSQTPMPQRPVEPQEGPHK-----SLQDQF	586
Db	542	PEPPIQASPGPPGPLSQTPMPQRPVEPQEGPHKSLVAHRVPLKPYAAPVPRSQSLQDQF	601
Qy	587	TRNLAAFPASHDDPAIPAPTATPSARGAVIRQNSDPTSEGPGSPNPPPAWVRPDNEAPP	646
Db	602	TRNLAAFPASHDDPAIPAPTATPSARGAVIRQNSDPTSEGPGSPNPPPAWVRPDNEAPP	661
Qy	647	KVPORTSSIATALNTSGAGGSRPAQAVRARPRSNSAWQIYLQRRRAERGTPKPPGPPAOPP	706
Db	662	KVPORTSSIATALNTSGAGGSRPAQAVRARPRSNSAWQIYLQRRRAERGTPKPPGPPAOPP	721
Qy	707	GPPNASSNPDLRRSDPGWERSDSVLPASHGHLPAQAGSLERNRVGASSKLDSSPVLSPGNK	766
Db	722	GPPNASSNPDLRRSDPGWERSDSVLPASHGHLPAQAGSLERNRVGVSSKDPSSPVLSPGNK	781
Qy	767	AKPDDHRSRPRGPADFVLLKERTLDEAPRPKKAMDYSSSSSEEVESSEDEEEGEGGPAE	826
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Qy	1067	LSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPK	1126
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Db	1201	QSQITPHAIIFLPNTDGMEMLLCYEDEGVVNTYTGRIKDVVLQNGEMPTSVAYICSNQI	1260
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Db	1261	MGWGEKAIEIRSVETGHLDGVMHKAQRLKFLCERNDKVFFASVRSGGSSQVYFMTLNR	1320
Qy	1307	NCIMNW 1312	
Db	1321	NRIMNW 1326	



Applicants Copy

REFERENCE  
NINTHORS  
2 (bases 1 to 388)  
Don T. Watanabe M V and Associates A

Query Match	96.3%;	Score 3803.2;	DB 1;	Length 3888;
Best Local Similarity	95.6%;	Pred. No. 0;		
Matches 3825;	Conservative 0;	Mismatches 3;	Indels 171;	Gaps 2;
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RESULT 2
us-09-688-188b-11

Query Match 95.8%; Score 3785; DB 2; Length 4133;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 3824; Conservative 0; Mismatches 15; Indels 150; Gaps 3;
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Qy 2063 ATCTGCAAGCGCGGAGAGCGGGGCAACCCAAAGCTTCCAGGGCCCCCTGTGTCAGCCCC 2122  
Db 2102 ATCTGCAAGCGCGGAGAGCGGGGCAACCCAAAGCTTCCAGGGCCCCCTGTGTCAGCCCC 2161  
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Job time : 23 secs



3 Mon Aug 30 09:54:26 2004

us-10-02

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Qy      1301  FMTLNRNCIMNW 1312
Db      1321  |||||FMTLNRNCIMNW 1332
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OM protein - protein search, using sw model

Run on: August 28, 2004, 00:54:25 ; Search time 35 Seconds  
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1935.236 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

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Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	6659	96.1	1326	4	US-09-688-188B-15
2	6659	96.1	1326	4	US-09-291-417D-14
3	4370.5	63.1	1324	4	US-09-645-456A-13
4	4370.5	63.1	1324	4	US-09-425-324A-13
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6	4360.5	62.9	1332	4	US-09-645-456A-9
7	4360.5	62.9	1332	4	US-09-425-324A-9
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15	4336	62.6	1360	4	US-09-425-324A-34
16	4336	62.6	1360	4	US-09-645-791-34
17	4274	61.7	1269	4	US-09-645-456A-15
18	4274	61.7	1269	4	US-09-425-324A-15
19	4274	61.7	1269	4	US-09-645-791-15
20	4264	61.5	1277	4	US-09-645-456A-12
21	4264	61.5	1277	4	US-09-425-324A-12
22	4264	61.5	1277	4	US-09-645-791-12
23	4249.5	61.3	1298	4	US-09-645-456A-14
24	4249.5	61.3	1298	4	US-09-425-324A-14
25	4249.5	61.3	1298	4	US-09-645-791-14
26	4239.5	61.2	1306	4	US-09-645-456A-10
27	4239.5	61.2	1306	4	US-09-425-324A-10

Sequence 10, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 89, Appl  
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Sequence 35, Appl  
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Sequence 88, Appl  
Sequence 88, Appl  
Sequence 105, App  
Sequence 105, App  
Sequence 8, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 14, Appl

## ALIGNMENTS

### RESULT 1

US-09-688-188B-15  
; Sequence 15, Application US/09688188B  
; Patent No. 6656716

; GENERAL INFORMATION:

; APPLICANT: PLOWMAN, GREGORY

; APPLICANT: MARTINEZ, RICARDO

; APPLICANT: WYTE, DAVID

; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

; FILE REFERENCE: 038602/0328

; CURRENT APPLICATION NUMBER: US/09/688,188B

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 09/291,417

; PRIOR FILING DATE: 1999-04-14

; PRIOR APPLICATION NUMBER: 65/081,784

; NUMBER OF SEQ ID NOS: 155

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 15

; LENGTH: 1326

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-688-188B-15

Query Match 96.1%; Score 6659; DB 4; Length 1326;

Best Local Similarity 95.8%; Pred. No. 0;

Matches 1270; Conservative 3; Mismatches 3; Indels 50; Gaps 3;

Oy 36 YGQVYGRHVKTGQLAAIKVMDVTEDEEEIKOEINMLKKYSHRNATYVGAFIKKSP 95

Db 2 FGVEYGRHVKTGQLAAIKVMDVTEDEEEIKOEINMLKKYSHRNATYVGAFIKKSP 61

Oy 96 GNDQLWLVNMFPGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHVHAHVHDIK 155

Db 62 GNDQLWLVNMFPGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHVHAHVHDIK 121

Oy 156 GQNVLLTENAENVKLVFGVSAQLDRTVGRNTFTGTPYMAPEVIACDENPDATYD 215

Db 122 GQNVLLTENAENVKLVFGVSAQLDRTVGRNTFTGTPYMAPEVIACDENPDATYD 181

Oy 216 IWSLGTATLWMAAGAPLCLDMHPRALFLIPNPPRLSKKWSKFFIDTCLIKTYL 275

Db 182 IWSLGTATLWMAAGAPLCLDMHPRALFLIPNPPRLSKKWSKFFIDTCLIKTYL 241

Oy 276 SRPPTQLLKFPPIRDQPTQVRIQLKHIDRSRKRGEKEETEYVSGSEEDDSHGE 335

Db 242 SRPPTQLLKFPPIRDQPTQVRIQLKHIDRSRKRGEKEETEYVSGSEEDDSHGE 301

Oy 336 EGFPSSIMNVPGESTLRREFLRLOQNKNSALQQOQOQOQDPEAHIKLLHQRQ 395

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OM protein - protein search, using sw model

Run on: August 28, 2004, 00:43:18 ; Search time 154 Seconds  
(without alignments)

2407.158 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	6659	96.1	1326	2 AAY55933	Human ZC3
4	6646.5	95.9	1303	4 AAM79153	Human pro
5	6646.5	95.9	1303	5 AAO18507	Human ins
6	6628.5	95.7	1303	4 AAO18507	Human ins
7	6622	95.6	1332	4 AAE10612	Human nov
8	6603.5	95.3	1376	7 ADE34154	Human nov
9	6311	91.1	1244	4 AAE10614	Human mis
10	6304.5	91.0	1273	4 AAE10613	Human nov
11	5651	81.6	1701	4 ABG24020	Novel hum
12	4370.5	63.1	1324	4 AAB68221	Amino aci
13	4360.5	62.9	1332	4 AAB68217	Amino aci
14	4346	62.7	1353	4 AAB68219	Amino aci
15	4336	62.6	1360	3 AAB85263	Amino aci
16	4336	62.6	1360	4 AAB50059	Human pro
17	4336	62.6	1360	5 AAO18506	Large NIK
18	4336	62.6	1385	7 AAD14162	Human ins
19	4325	62.4	1385	4 AAM79405	Human src
20	4274	61.7	1268	7 ADE31765	Human pro
21	4274	61.7	1269	4 AAB68223	Human 154
22	4264	61.5	1277	4 AAB68220	Amino aci
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24	4244	61.2	1339	4 AAM78421	Human pro
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26	4195.5	60.5	1297	2 AAY55932	Human ZC2
27	4021.5	58.0	1239	2 AAY55931	Human ZC1
28	3977	57.4	1212	4 AAE04368	Human kin
29	3977	57.4	1212	7 ADE35753	Human pro
30	3960.5	57.2	1165	3 AAB43016	Human pro
31	3951.5	57.0	1233	2 AAY55954	Mouse ORF
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36	3824	55.2	1175	5 AAU76512	Human HPK
37	3821	55.1	1792	7 ADE34152	Human mis
38	3807.5	55.0	1655	4 ABG17466	Novel hum
39	3777.5	54.3	1135	3 AAY68784	Amino aci
40	3694.5	53.5	1219	4 ABG17469	Novel hum
41	2708.5	39.1	1109	2 AAY55953	Human pro
42	2280	32.9	510	3 AAB54144	Human pan
43	1862.5	26.9	1227	2 AAY55965	Full leng
44	1819.5	26.3	1581	5 AAE24145	Human kin
45	1686	24.3	425	4 AAB92792	Human pro

#### ALIGNMENTS

##### RESULT 1

ADE34150  
ID ADE34150 standard; protein; 1312 AA.

XX ADE34150;

XX 29-JAN-2004 (first entry)

XX Human mishapen/NIKS-related kinase, Mink3a.

XX Human; mishapen/NIKS-related kinase; Mink3a; enzyme; antiinflammatory;  
XX immunosuppressive; cytostatic; germinal centre kinase;  
XX c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;  
XX growth factor induced-ERK activation; proliferation;  
XX cell proliferation disorder; cell survival;  
XX intracellular signal transduction; apoptosis; morphological change;  
XX cell migration; gene therapy; inflammatory disease; autoimmune disease;  
XX immunodeficiency; cancer.

XX Homo sapiens.

XX US2003077597-A1.

XX 24-APR-2003.

XX 19-OCT-2001; 2001US-00029115.

XX 19-OCT-2001; 2001US-00029115.

XX (LUOY/) LUO Y.

XX (FUCA/) FU C A.

XX (SHEN/) SHEN M.

XX Luo Y, Fu CA, Shen M;

XX WPI; 2003-635076/60.

XX N-PSDB; ADE34151.

XX New mishapen/NIKS-related kinase nucleic acids and proteins useful in

XX gene therapy and for treating disorders, e.g. acute and chronic

XX Claim 5; SEQ ID NO 2; 53pp; English.

XX The invention relates to a recombinant nucleic acid capable of

XX hybridising to a Human DNA encoding mishapen/NIKS-related kinase

XX (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as

XX ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or

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3	4336	62.6	1360	1	TN1K HUMAN
4	4017.5	58.0	1239	1	M4K4 HUMAN
5	3951.5	57.0	1233	1	M4K4 MOUSE
6	3286	47.4	916	1	TN1K MOUSE
7	2646	38.2	1080	1	M115 HUMAN
8	738	10.7	894	1	M4K3 CARBL
9	729	10.5	862	1	M4K3 RAT
10	715.5	10.3	487	1	STK4 HUMAN
11	694.5	10.0	491	1	STK3 HUMAN
12	693.5	10.0	669	1	HPO HUMAN
13	691	10.0	847	1	M4K5 MOUSE
14	687	9.9	846	1	M4K5 HUMAN
15	681.5	9.8	426	1	ST25 MOUSE
16	675.5	9.7	426	1	ST25 HUMAN
17	667	9.6	1080	1	NRK1 YEAST
18	660.5	9.5	833	1	M4K1 HUMAN
19	656.5	9.5	443	1	ST24 HUMAN
20	853.5	9.4	819	1	M4K2 HUMAN
21	644	9.3	968	1	STK4 HUMAN
22	638	9.2	821	1	M4K2 MOUSE
23	636.5	9.2	966	1	STK4 MOUSE
24	630.5	9.1	681	1	M4K3 MOUSE
25	629	9.1	827	1	M4K1 MOUSE
26	620.5	9.0	1501	1	N1NC DROME
27	552	8.0	471	1	SID1 SCHPO
28	551	8.0	982	1	SULU CARBL
29	548	7.9	490	1	SPS1 YEAST
30	532.5	7.7	658	1	PAK1 SCHPO
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77	504	7.3	556	1	SPAK MOUSE
78	504	7.3	556	1	SPAK MOUSE
79	504	7.3	556		

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OM protein - protein search, using sw model

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Title: US-10-029-115-2  
Perfect score: 6929  
Sequence: 1 MGDPAPARSLDIDLALRD.....SGSSQVYFWTLNRCNMW 1312

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- SPTRMBL\_25:\*
  - 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_muc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_virus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archepa:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6701	96.7	1334	11 Q7TT13	Q7TT13 mus musculus
2	4189.5	60.5	1303	13 Q7SY42	Q7SY42 brachydanio
3	2805.5	40.5	1550	5 Q9W002	Q9W002 drosophila
4	2698	38.9	1082	5 Q8T8M3	Q8T8M3 caenorhabdi
5	2696.5	38.9	1087	5 Q9XYC3	Q9XYC3 caenorhabdi
6	2692	38.9	1096	5 Q95217	Q95217 caenorhabdi
7	2661	38.4	1072	5 Q814B5	Q814B5 caenorhabdi
8	1855	26.8	538	4 Q7Z4L4	Q7Z4L4 homo sapien
9	1826	26.4	1582	4 Q7Z2Y5	Q7Z2Y5 homo sapien
10	1702.5	24.6	1455	11 Q9R0G8	Q9R0G8 mus musculus
11	1701.5	24.6	1455	11 Q9R0S4	Q9R0S4 mus musculus
12	1551	22.4	292	4 Q9HMG9	Q9HMG9 homo sapien
13	1458	21.0	792	5 Q9UAN7	Q9UAN7 caenorhabdi
14	1377	19.9	728	5 Q9XYC4	Q9XYC4 caenorhabdi
15	993	14.3	334	11 Q8C9S9	Q8C9S9 mus musculus
16	829.5	12.0	169	11 Q61155	Q61155 mus musculus

- Q9V8r6 drosophila
- Q9ny8s homo sapien
- Q8nev4 homo sapien
- Q8k3h5 mus musculus
- Q90xg6 brachydanio
- Q9d888 morone saxa
- Q800q6 morone saxa
- Q81x64 homo sapien
- Q81x68 homo sapien
- Q81x65 homo sapien
- Q8wxr4 homo sapien
- Q81x66 homo sapien
- Q81x67 homo sapien
- Q8en94 homo sapien
- Q861x1 dictyosteli
- Q871h9 neurospora
- Q8sael triticum mo
- Q9arl7 hordeum vul
- Q9j111 mus musculus
- Q9yhc9 xenopus lae
- Q9fnu3 oryza sativ
- Q24527 arabidopsis
- Q91qai arabidopsis
- Q802a6 squalus aca
- Q9j110 mus musculus
- Q800g4 mus musculus
- Q8syai drosophila
- Q952h6 caenorhabdi
- Q9ml18 drosophila

ALIGNMENTS

RESULT 1

- ID Q7TT13 PRELIMINARY; PRT; 1334 AA.
- AC Q7TT13;
- DT 01-OCT-2003 (TrEMBLrel. 25, Created)
- DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
- DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
- DE Hypothetical protein.
- OS Mus musculus (Mouse).
- OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
- OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
- OX NCBI\_TaxID=10090;
- RN [1]
- RP SEQUENCE FROM N.A.
- RC STRAIN=C57BL/6; TISSUE=Brain;
- RX MEDLINE=22388257; PubMed=12477932;
- RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Farber A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
- RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
- RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
- RP SEQUENCE FROM N.A.
- RC STRAIN=C57BL/6; TISSUE=Brain;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 00:52:04 ; Search time 53 seconds  
(without alignments)  
2381.194 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

Sequence: 1 MGDPAPARSLDDIDLSALRD.....SGSGSQVYFMTLNRNCIMNW 1312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3951.5	57.0	1233	2	T30989	serine/threonine p
2	3008.5	43.4	1102	2	JC8316	probable protein k
3	2647.5	38.2	1075	2	T27622	hypothetical prote
4	2646	38.2	1080	2	T27622	hypothetical prote
5	2403.5	34.7	1027	2	T46481	hypothetical prote
6	1458	21.0	792	2	T43630	serine/threonine p
7	1377	19.9	728	2	T43632	serine/threonine p
8	710	10.2	836	2	B96716	probable serine/th
9	698	10.1	653	2	T34356	hypothetical prote
10	688.5	9.9	1233	2	T1457	serine/threonine p
11	678.5	9.8	426	2	S71886	Ste20-like protein
12	670	9.7	1231	2	T18532	serine/threonine pr
13	667	9.6	1080	2	S48944	hypothetical prote
14	658	9.5	1001	2	T17365	serine/threonine p
15	653.5	9.4	819	2	A53714	protein kinase (EC
16	651.5	9.4	1206	2	T34021	protein kinase SK2
17	640.5	9.2	829	2	T29372	hypothetical prote
18	635.5	9.2	690	2	C96572	protein F12M16.4 (
19	616.5	8.9	1135	1	A29813	132K ninaC protein
20	616.5	8.9	1501	1	T29913	174K ninaC protein
21	588.5	8.5	1228	2	T18897	hypothetical prote
22	582.5	8.4	1014	2	T31109	myosin III - Atlan
23	552	8.0	471	2	T39232	probable serine th
24	551	8.0	982	2	T18576	serine-threonine k
25	548	7.9	490	2	S47946	protein kinase hom
26	535	7.7	312	2	T38525	serine/threonine p
27	533.5	7.7	658	2	T39500	serine/threonine-s
28	505	7.3	652	2	T39722	serine/threonine p
29	504.5	7.3	658	2	S60170	protein kinase fak

30	501.5	7.2	561	2	T51417	protein kinase-lik
31	498.5	7.2	544	2	A57597	beta-p21-activated
32	497	7.2	710	2	T13458	hypothetical prote
33	496	7.2	544	2	S40482	serine/threonine-s
34	496	7.2	545	2	G01773	p21-activated prot
35	495.5	7.2	842	2	S60402	protein kinase CLA
36	493.5	7.1	544	2	I49376	p21 activated kina
37	489	7.1	553	2	T01479	hypothetical prote
38	488	7.0	589	2	T38066	serine/threonine-p
39	481.5	6.9	525	2	S58682	protein kinase, p2
40	478.5	6.9	622	2	T15467	hypothetical prote
41	478.5	6.9	655	2	S51884	probable protein k
42	474.5	6.8	378	2	T26684	hypothetical prote
43	463	6.7	693	2	B85112	hypothetical prote
44	459	6.6	939	2	S28394	probable serine/th
45	455	6.6	607	2	T01904	hypothetical prote

ALIGNMENTS

RESULT 1

T30989

serine/threonine protein kinase NIK - mouse

N/Alternate names: NCK interacting kinase

C/Species: Mus musculus (house mouse)

C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999

C/Accession: T30989

R/Su. Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y.

EMBO J. 16, 1279-1290, 1997

A/Title: NIK is a new Ste20-related kinase that binds NCK and MEK1 and activates the

A/Reference number: Z20954; MUID:97280817; PMID:9135144

A/Accession: T30989

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1233 <SU>

A/Cross-references: EMBL:U88984; NID:g1872545; PID:g1872546; PIDN:AAC53165.1

C/Keywords: protein kinase

Query Match	57.0%	Score	3951.5	DB	2	Length	1233;
Best Local Similarity	62.3%	Pred. No.	1.8e-105;				
Matches	846;	Conservative	112;	Mismatches	228;	Indels	173;
Gaps	32;						
Qy	1	MGDPAPARSLDDIDLSALRD	PAGIFELVEVNGT	YGVYKGRHVT	QGLAAIKWMDVTE	60	
Db	1	MANDSPAKSLVDIDLSLRDP	PAGIFELVEVNGT	YGVYKGRHVT	-VTAAIKWMDVTE	59	
Qy	61	DEEEIKQEIINMLKKYSHRN	NIATYTGAFIKKPP	GGNDQDLWLMFPCG	AGSVTDLVKNT	120	
Db	60	DEEEITLEINMLKKYSHRN	NIATYTGAFIKKPP	GGDDQDLWLMFPCG	AGSITDLVNT	119	
Qy	121	KGNALEDCTIATCRILRGL	AHLHAKVTHRDIK	QNVLLTENAEVKLV	DVGVSQALDR	180	
Db	120	KGNTLKEDWIATSRILRGL	AHLHAKVTHRDIK	QNVLLTENAEVKLV	DVGVSQALDR	179	
Qy	181	TVGRRTFTGTPVWMAPEVI	ACDENPDATYVRS	DTWSLGITAIEMAE	GPICDMHPR	240	
Db	180	TVGRRTFTGTPVWMAPEVI	ACDENPDATYVRS	DLWSCGITAIEMAE	GPICDMHPR	239	
Qy	241	ALFLIPRNPPLKSKKSKK	FFIDTDTCLITK	YLSRPPTEQLLKPF	FPIDQPTQVRI	300	
Db	240	ALFLIPRNPPLKSKKSKK	FFIEGCLVKNYMR	QPSFTEQLLKPF	FPIDQPTQVRI	299	
Qy	301	QLKDHIDRKKKGEKEETE	YYSGSEEDDSHG	E-EGPSSIMNVPG	ESTURRFLRIQ	359	
Db	300	QLKDHIDRKKKGEKEETE	YYSGSEEDDSHG	E-EGPSSIVNVPG	ESTURRFLRIQ	359	
Qy	360	QENKSNSEALKQOQQOQ	QOQDPPEAHIKH	LHQRIIEEKEERR	VEEQRREOR	419	
Db	360	QENKSNSEALKQOQQOQ	QOQDPPEAHIKH	LHQRIIEEKEERR	VEEQRREOR	419	
Qy	420	KLEKEQ-----QRLED	MQALPR-----	BEERRQAEQYRKQ	L-EQROSE	463	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 00:57:10 ; Search time 81 Seconds  
(without alignments)  
5095.952 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

Sequence: 1 MGDPAKSLDDIDLSALRD.....SGSSQVYFMTLNRCINMW 1312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US05\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6929	100.0	1312	14	US-10-029-115-2
2	6660.5	96.1	1295	10	US-09-789-390-30
3	6660.5	96.1	1295	10	US-09-789-390-32
4	6660.5	96.1	1295	10	US-09-789-390-34
5	6660.5	96.1	1295	10	US-09-789-390-37
6	6660.5	96.1	1295	10	US-09-789-390-39
7	6659	96.1	1326	10	US-09-291-417-15
8	6646.5	95.9	1303	10	US-09-789-390-35
9	6646.5	95.9	1303	10	US-09-789-390-38
10	6628.5	95.7	1303	10	US-09-789-390-7
11	6622	95.6	1332	10	US-09-789-390-9
12	6603.5	95.3	1276	14	US-10-029-115-6
13	6311	91.1	1244	10	US-09-789-390-13
14	6304.5	91.0	1273	10	US-09-789-390-11
15	5422.5	78.3	1303	10	US-09-789-390-65

16	5412	78.1	1332	10	US-09-789-390-63	Sequence 63, Appl
17	5261	75.9	1244	10	US-09-789-390-70	Sequence 70, Appl
18	5261	75.9	1244	10	US-09-789-390-71	Sequence 71, Appl
19	5250.5	75.8	1273	10	US-09-789-390-67	Sequence 67, Appl
20	5250.5	75.8	1273	10	US-09-789-390-68	Sequence 68, Appl
21	4336	62.6	1360	9	US-09-871-916-2	Sequence 2, Appl
22	4336	62.6	1360	14	US-10-355-975-14	Sequence 14, Appl
23	4274	61.7	1268	15	US-10-353-690-122	Sequence 122, Appl
24	4195.5	60.5	1297	10	US-09-291-417-14	Sequence 14, Appl
25	4021.5	58.0	1239	10	US-09-291-417-13	Sequence 13, Appl
26	3977	57.4	1212	12	US-10-168-582-9	Sequence 9, Appl
27	3977	57.4	1212	14	US-10-247-671-157	Sequence 157, Appl
28	3951.5	57.0	1233	10	US-09-291-417-89	Sequence 89, Appl
29	3872.5	55.9	1165	12	US-10-211-462-89	Sequence 89, Appl
30	3872.5	55.9	1165	14	US-10-021-660-126	Sequence 126, Appl
31	3824	55.2	1175	9	US-09-771-161A-224	Sequence 224, Appl
32	3824	55.2	1175	9	US-09-771-161A-225	Sequence 225, Appl
33	3824	55.2	1175	9	US-09-771-161A-226	Sequence 226, Appl
34	3821	55.1	792	14	US-10-029-115-4	Sequence 4, Appl
35	2708.5	39.1	1109	10	US-09-291-417-88	Sequence 88, Appl
36	2403.5	34.7	1027	16	US-10-408-765A-1181	Sequence 1181, Appl
37	2280	32.9	510	9	US-09-925-297-596	Sequence 596, Appl
38	1862.5	26.9	1227	10	US-09-291-417-105	Sequence 105, Appl
39	1819.5	26.3	1581	12	US-10-415-011-16	Sequence 16, Appl
40	1797	25.9	515	9	US-09-771-161A-134	Sequence 134, Appl
41	1686	24.3	425	9	US-09-771-161A-133	Sequence 133, Appl
42	1676.5	24.2	468	9	US-09-771-161A-135	Sequence 135, Appl
43	1600.5	23.1	339	16	US-10-664-421-79	Sequence 79, Appl
44	1532	22.1	288	12	US-10-276-774-1920	Sequence 1920, Appl
45	1457	21.0	275	14	US-10-355-975-8	Sequence 8, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-029-115-2  
; Sequence 2, Application US/10029115  
; Publication No. US20030077597A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Ying  
; APPLICANT: Shen, Mary  
; TITLE OF INVENTION: No. US20030077597A1 Germlinal Center Kinase Cell Cycle Protein  
; TITLE OF INVENTION: Methods of Use  
; FILE REFERENCE: A-70229/RMS/DHR  
; CURRENT APPLICATION NUMBER: US/10/029,115  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-115-2

Query Match	100.0%	Score	6929	DB 14	Length	1312
Best Local Similarity	100.0%	Pred. No.	4.4e-311			
Matches 1312	Conservative	0	Mismatches	0	Indels	0
Gaps	0					
Qy	1	MGDPAPARSLDDIDLSALRDPAGIFELVEVVGNGTYGVYKGRHVKTGQLAAIKVMDVTE	60			
Db	1	MGDPAPARSLDDIDLSALRDPAGIFELVEVVGNGTYGVYKGRHVKTGQLAAIKVMDVTE	60			
Qy	61	DEEETKQINMLKYSKSHRNATYTGAFIKSPGNDQDLWVMEFCAGSVTLVKNT	120			
Db	61	DEEETKQINMLKYSKSHRNATYTGAFIKSPGNDQDLWVMEFCAGSVTLVKNT	120			
Qy	121	KGNAKEDCIATYCREILGLAHKVIHDKQGVLLTENAELVDFGVSAQLDR	180			
Db	121	KGNAKEDCIATYCREILGLAHKVIHDKQGVLLTENAELVDFGVSAQLDR	180			
Qy	181	TGVRRTFTGTPTWMAPEVIACDENPDATYDYSRDSWLSLIGTATEMAEGAPPLCDMPMR	240			